

# Анализ и интерпретация Single-cell RNA-seq.

Dataset: 4k Pan T Cells from a  
Healthy Donor

## Действующие лица:

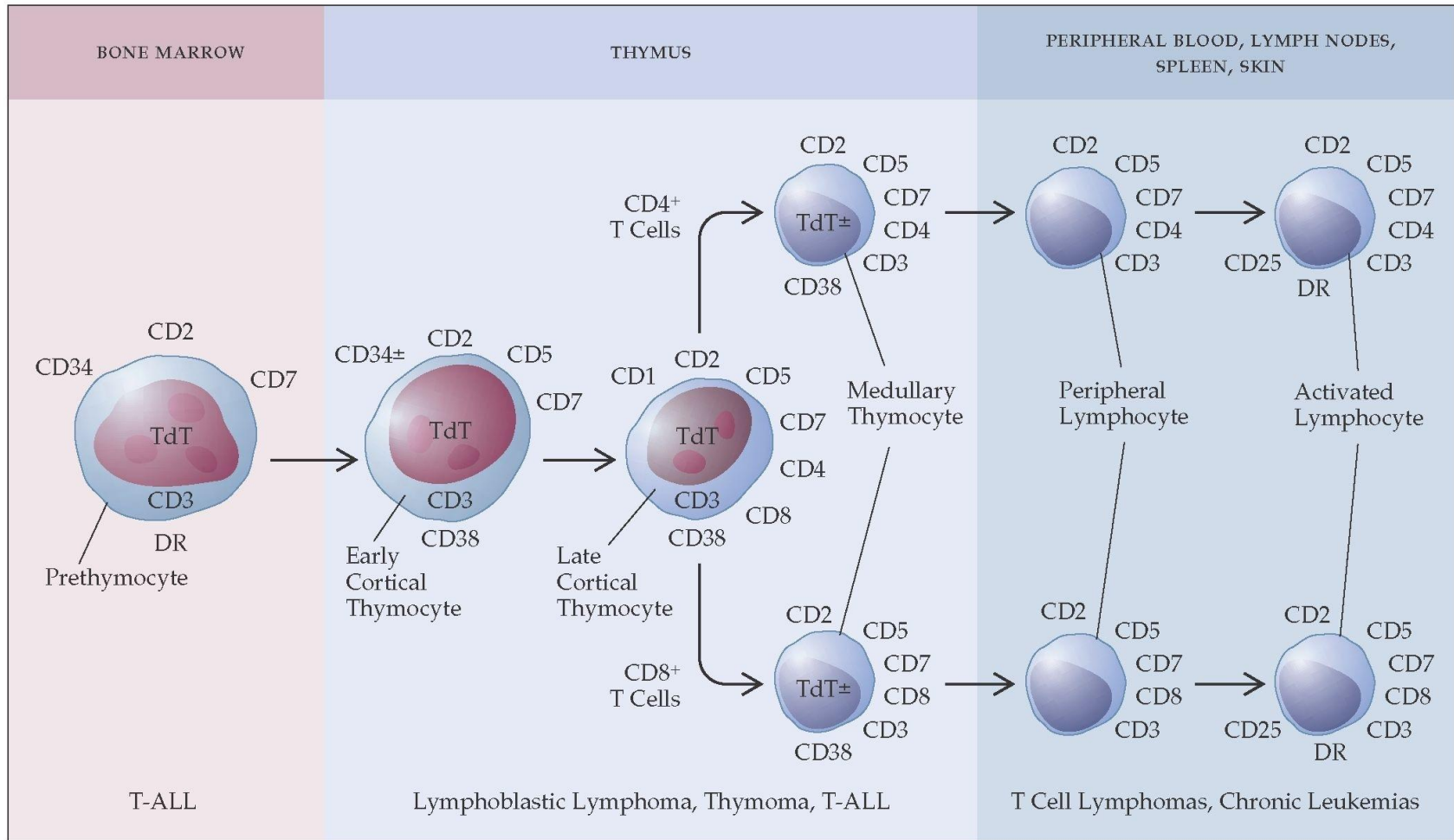
- 1) Анастасия Сокол (Б) – ревью-сечер, эксперт мемасер
- 2) Анастасия Котова (Б) - цитолог, гистолог, супер-хай-иммуно-интерпритер
- 3) Гузель Газизова (Б) – RNA-seq гениус
- 4) Дмитрий Орехов (Б/И) – ведущий разработчик
- 5) Семен Путников (И) – алгоритм дизайнер + математик
- 6) Колосов Никита (Б) – идейный вдохновитель

@// Вывод <- 75% биологизации

## Этапы работы:

- 1) Сбор материала
- 2) Теоретическое обоснование поставленной задачи
- 3) Примерное разделение ролей
- 4) Анализ данных и интерпретация
- 5) Результаты

# Задачи:



# Учи Матчасть!

Estimated Number of Cells

4,538

Mean Reads per Cell

73,864

Median Genes per Cell

1,067

## Sequencing

Number of Reads	335,198,537
Valid Barcodes	98.4%
Reads Mapped Confidently to Transcriptome	62.2%
Reads Mapped Confidently to Exonic Regions	65.8%
Reads Mapped Confidently to Intronic Regions	22.1%
Reads Mapped Confidently to Intergenic Regions	3.3%
Reads Mapped Antisense to Gene	3.3%
Sequencing Saturation	89.5%
Q30 Bases in Barcode	97.7%
Q30 Bases in RNA Read	79.5%
Q30 Bases in Sample Index	95.2%
Q30 Bases in UMI	97.8%

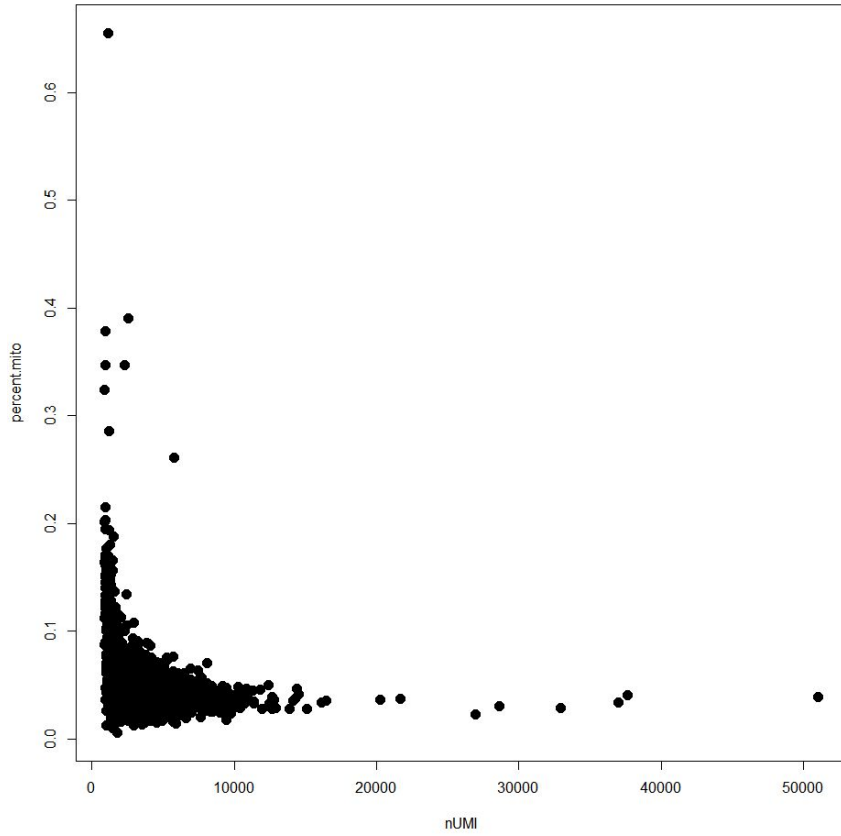
## Cells

Estimated Number of Cells	4,538
Fraction Reads in Cells	88.5%
Mean Reads per Cell	73,864
Median Genes per Cell	1,067
Total Genes Detected	18,920
Median UMI Counts per Cell	3,749

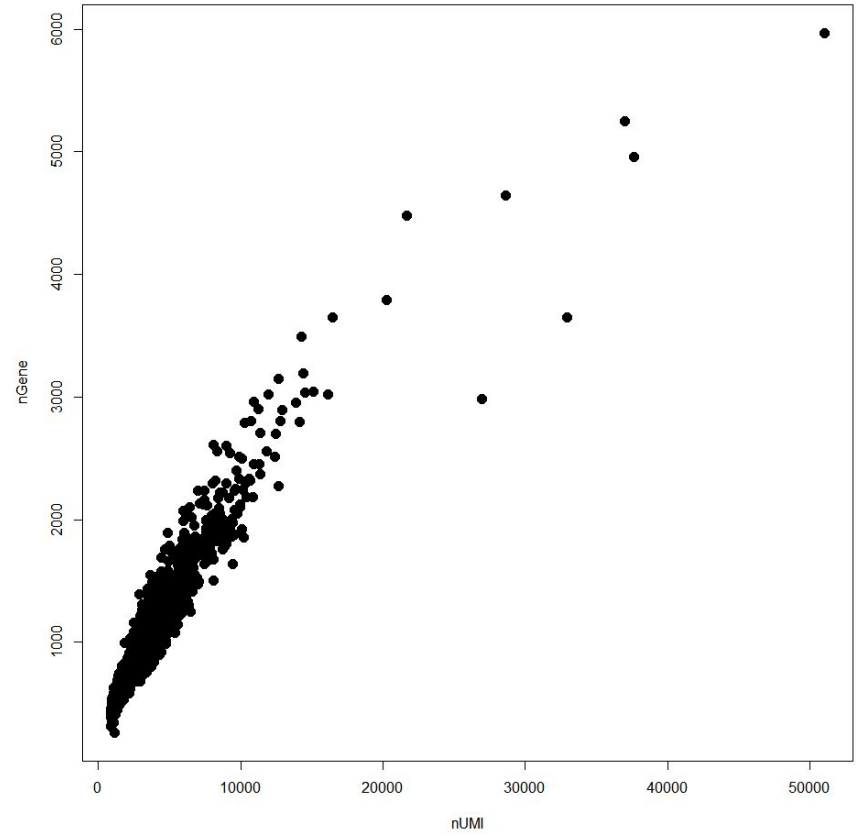
## Sample

Name	t_4k
Description	Pan T Cells isolated from mononuclear cells of a healthy donor
Transcriptome	GRCh38
Chemistry	Single Cell 3' v2
Cell Ranger Version	2.0.1

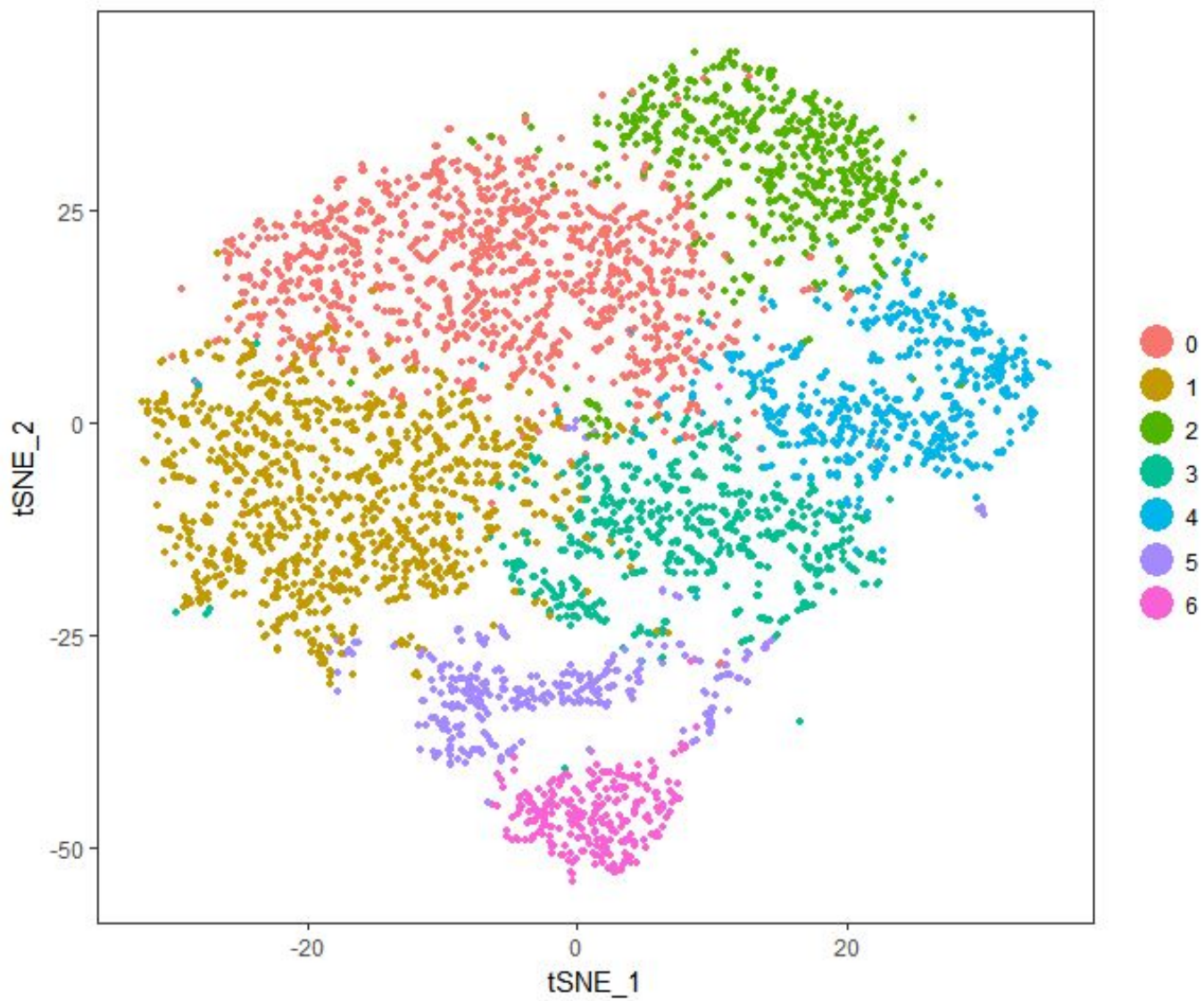
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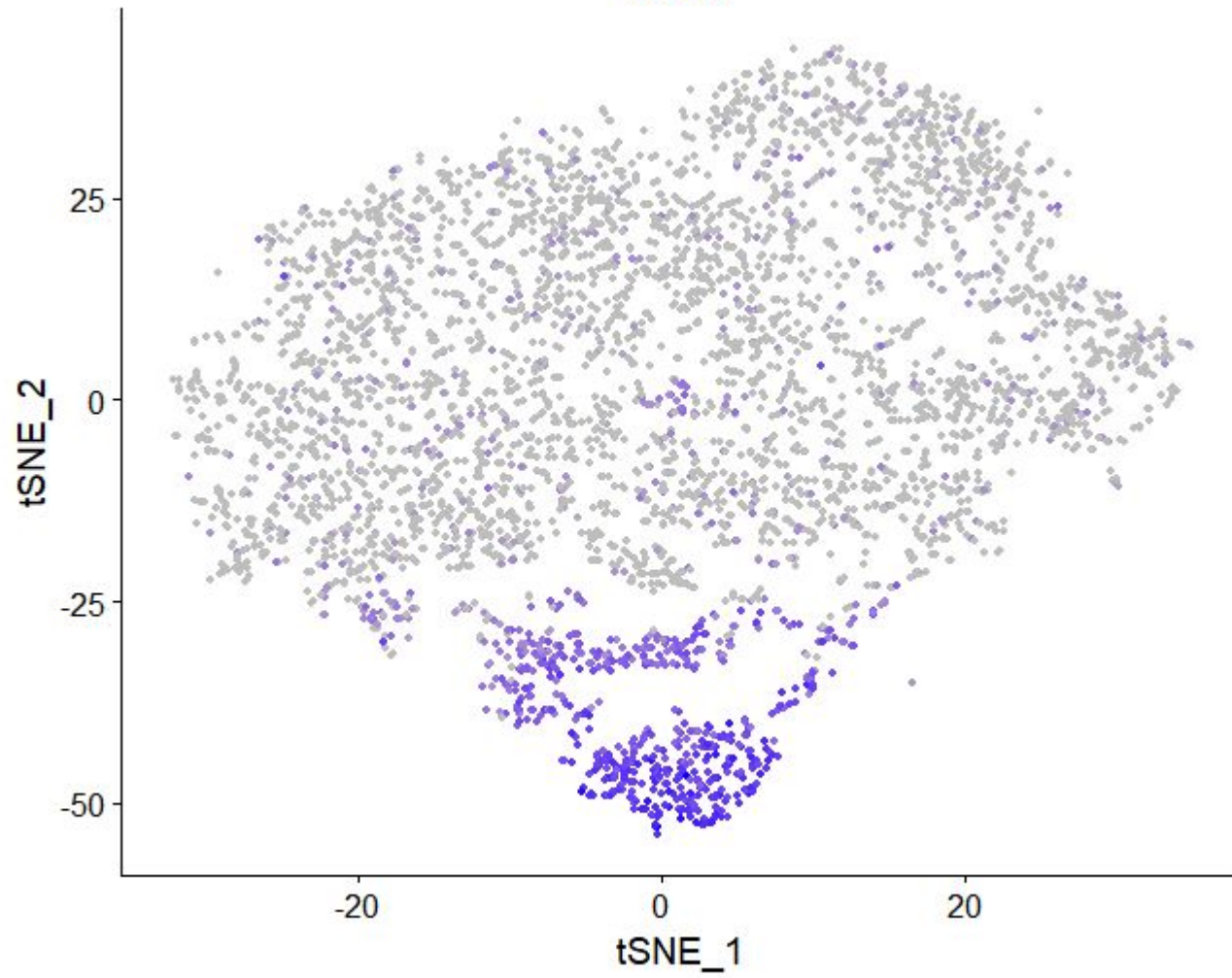
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Интерпретация:

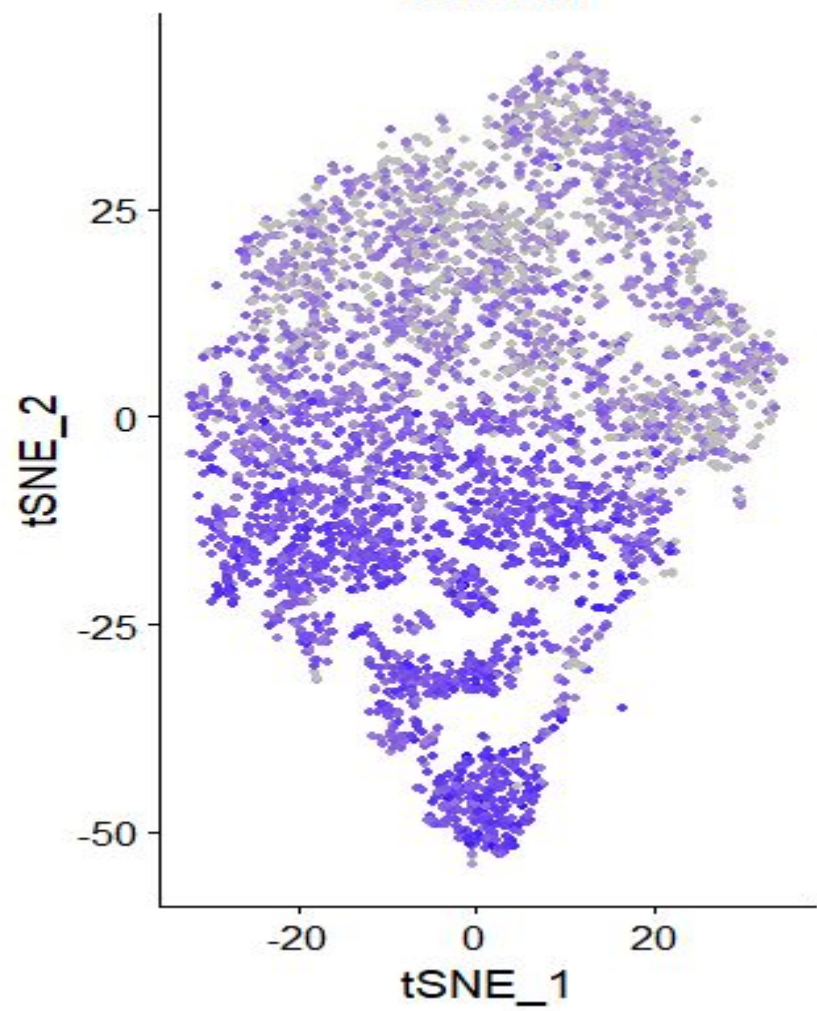


# NKG7

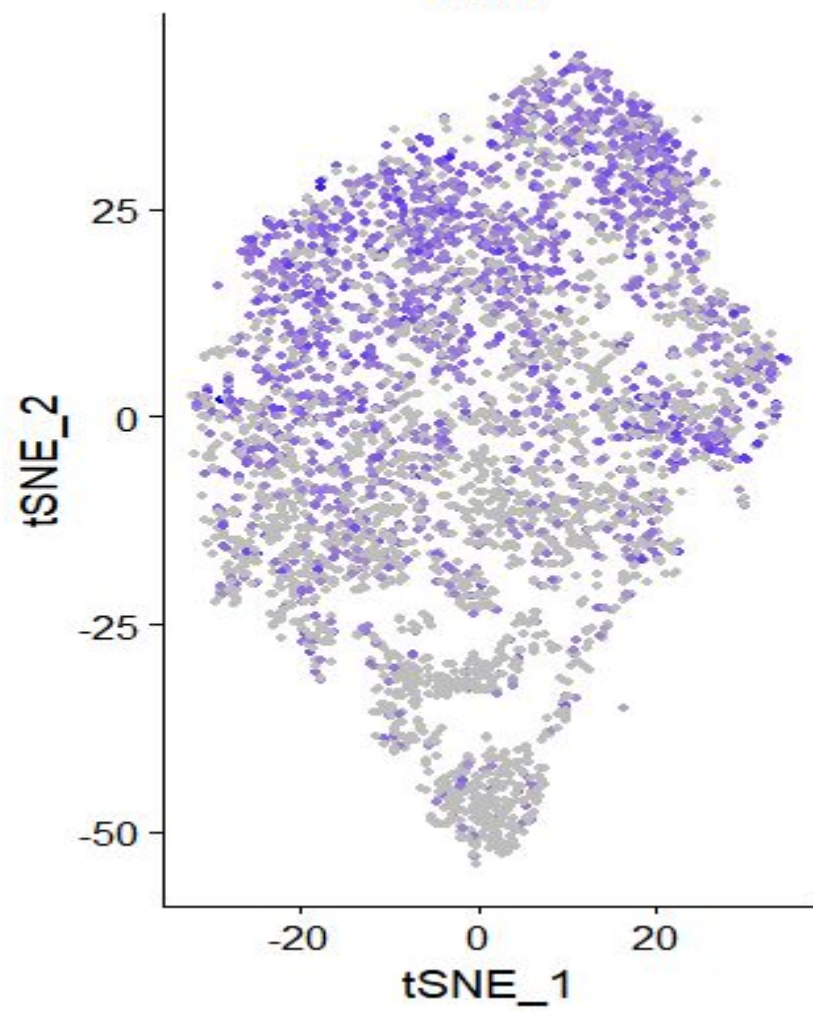




**S100A4**

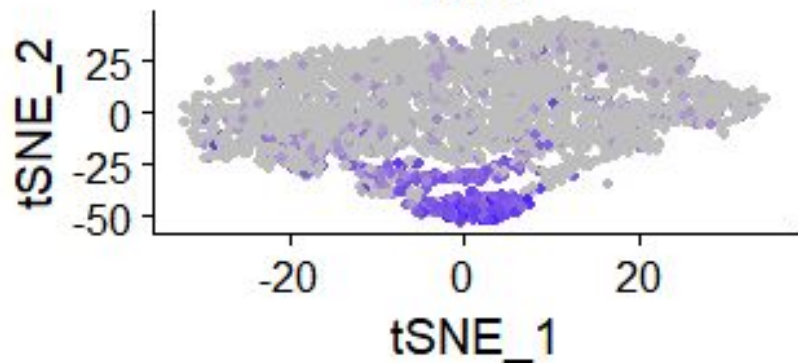


**CCR7**

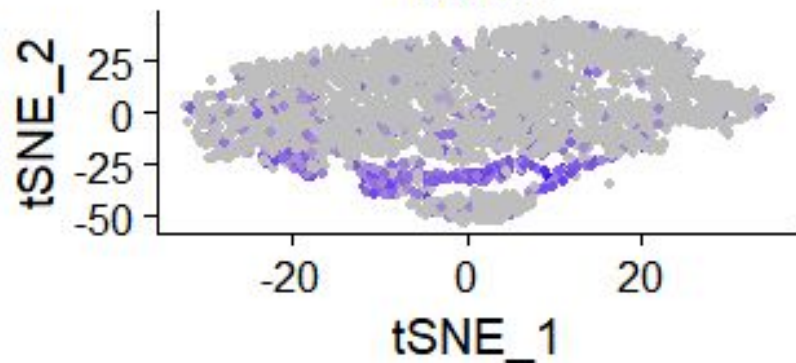




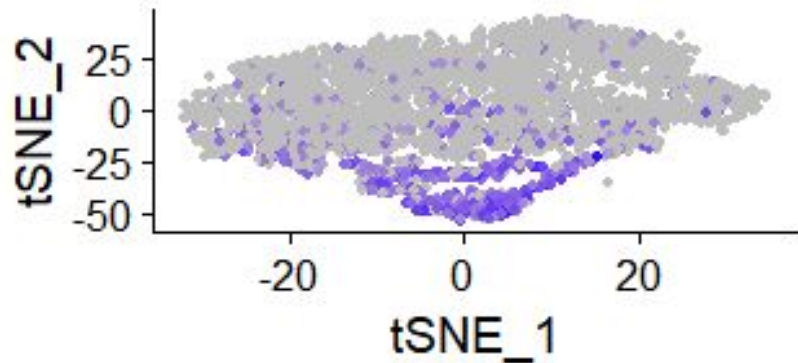
**GNLY**



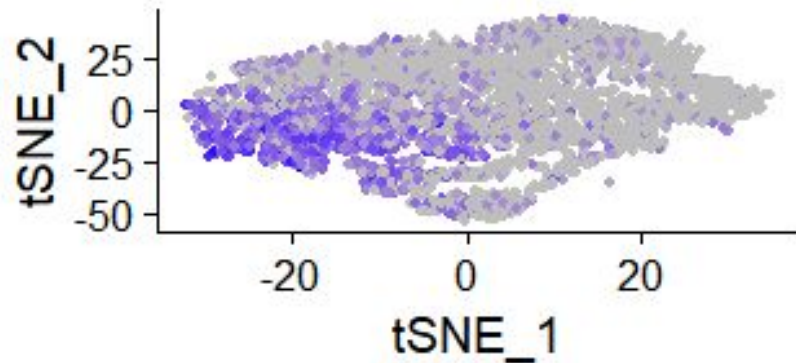
**GZMK**



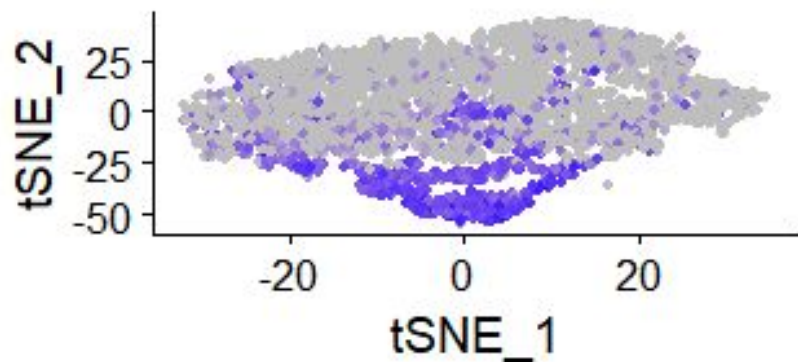
**GZMA**



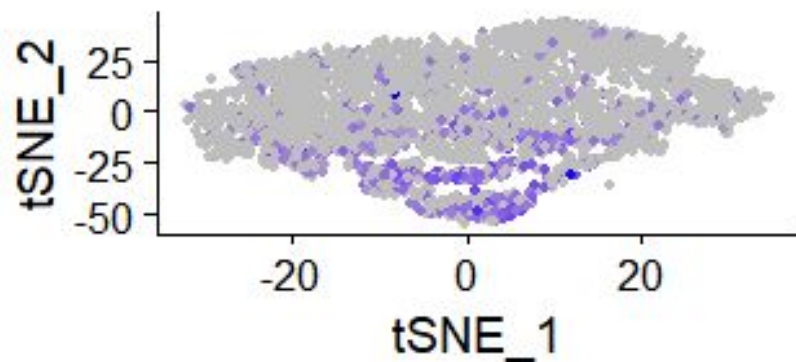
**LMNA**

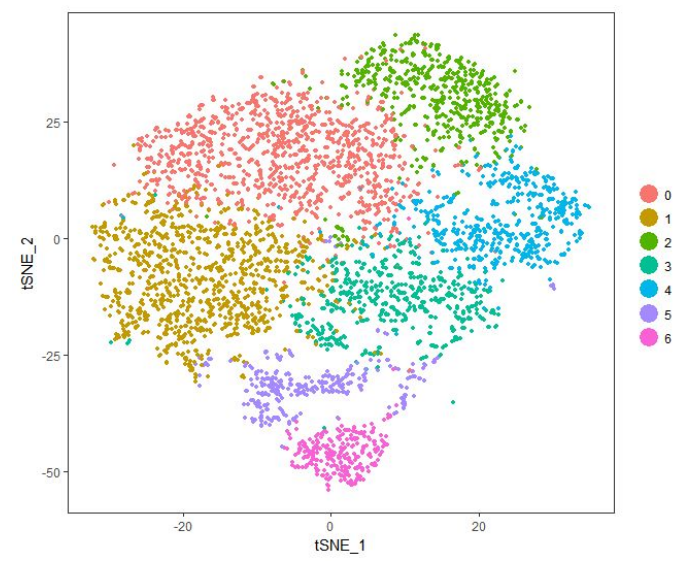
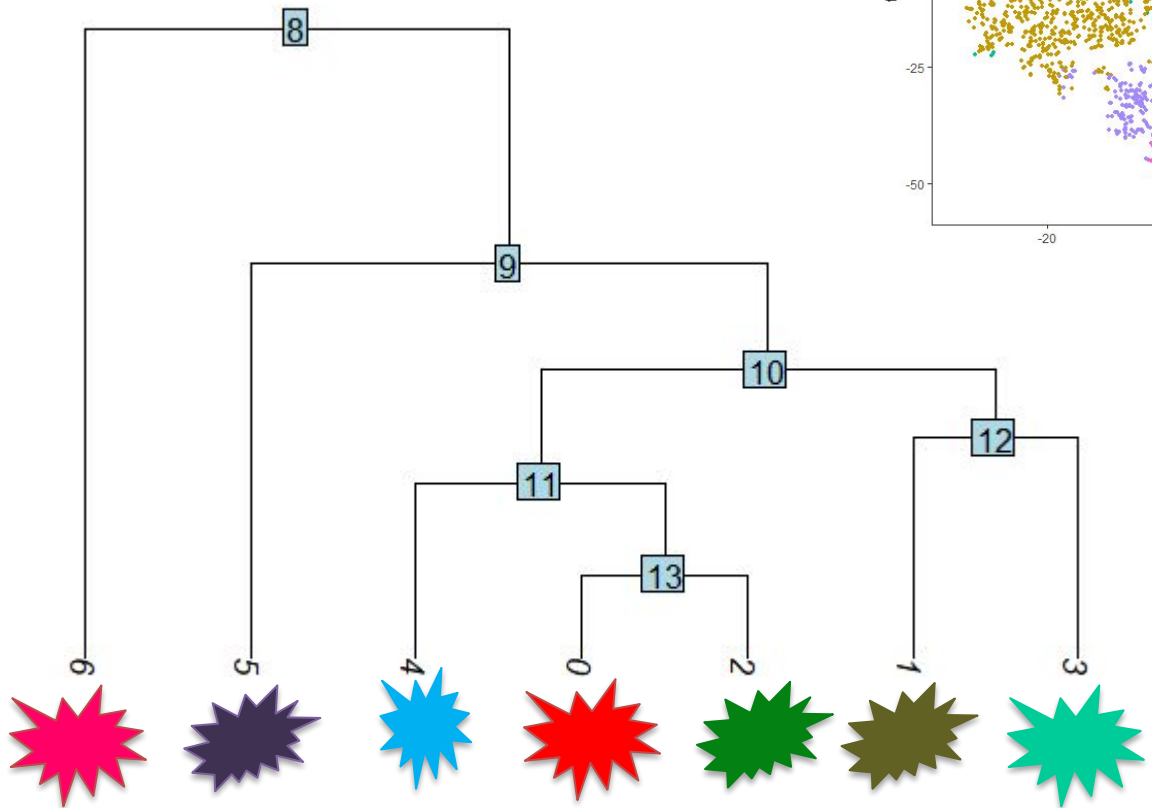


**CCL5**



**KLRG1**







American company:



Student:

